

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____

Art Unit: _____ Phone Number 30 _____ Serial Number: _____

Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

BEST AVAILABLE COPY

STAFF USE ONLY		Type of Search	Vendors and cost where applicable
Searcher:	_____	NA Sequence (#)	STN _____
Searcher Phone #:	_____	AA Sequence (#)	Dialog _____
Searcher Location:	_____	Structure (#)	Questel/Orbit _____
Date Searcher Picked Up:	3/3/01	Bibliographic	Dr.Link _____
Date Completed:	7/5/01	Litigation	Lexis/Nexis _____
Searcher Prep & Review Time:	_____	Fulltext	Sequence Systems <i>EV</i> _____
Clencal Prep Time:	_____	Patent Family	WWW/Internet _____
Online Time:	_____	Other	Other (specify) _____

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 4, 2001, 22:35:12 ; Search time 5349.06 Seconds

(without alignments)
9886.636 Million cell updates/sec

Title: US-09-117-447-1
Perfect score: 3687
Sequence: 1 atggatagaaaaaagctgt.....ttacattctatataaagtaa 3687

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 13641696 seqs, 711712690 residues

Total number of hits satisfying chosen parameters: 27283392

Minimum DB seq length: 0

Maximum DB seq length: 0

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_NA_Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3687	100.0	3687	15	US-09-117-447-1	Sequence 1, Appli
2	3687	100.0	3687	18	US-09-463-402-1	Sequence 1, Appli
3	3599	97.6	3768	18	US-09-463-402-12	Sequence 12, Appli
4	3598.2	97.6	4988	18	US-09-463-402-11	Sequence 11, Appli
5	3598	97.6	7814	54	US-60-226-176-1986	Sequence 11, Appli
6	71.4	1.9	7814	55	US-60-233-168-1986	Sequence 11, Appli
7	62.6	1.7	3579	1	PCP-US98-267-96-232	Sequence 232, App
8	58.8	1.6	957	18	US-09-457-659-2159	Sequence 2159, App
9	58.8	1.6	957	25	US-60-652-127-5964	Sequence 5964, App
10	57.8	1.6	3653	1	PCP-US98-12764-33	Sequence 33, Appli
11	57.6	1.6	186935	54	US-60-226-176-1976	Sequence 1976, App
12	57.6	1.6	186935	55	US-60-233-168-1976	Sequence 1976, App
13	56.8	1.5	4248	18	US-09-407-679-1	Sequence 1, Appli
14	54.6	1.5	22306	35	US-60-038-697-727	Sequence 727, App
15	54.6	1.5	2206	36	US-60-046-714-726	Sequence 726, App
16	53.8	1.5	8307	57	US-60-258-275-230	Sequence 230, App
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18	53	1.4	7253	16	US-08-268-347-35	Sequence 1, Appli
19	53	1.4	1830121	8	US-08-426-871-1	Sequence 1, Appli
20	53	1.4	1830121	8	US-08-476-102-1	Sequence 1, Appli
21	53	1.4	1830121	8	US-09-122-031B-312	Sequence 1, Appli
22	53	1.4	1830121	22	US-09-557-884-1	Sequence 1, Appli
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24	52.4	1.4	867	17	US-09-397-761A-2710	Sequence 2710, App
25	52.4	1.4	867	25	US-09-641-529-448	Sequence 448, App
26	52.2	1.4	666448	14	US-09-012-031B-312	Sequence 312, App
27	52.2	1.4	666448	14	US-09-012-031B-312	Sequence 312, App
28	52.2	1.4	666448	14	US-09-012-031C-312	Sequence 312, App
29	52.2	1.4	666448	17	US-09-335-032-12214	Sequence 1221, App
30	51.8	1.4	26	US-09-663-779-1221	Sequence 5, Appli	
31	51.8	1.4	35515	1	PCP-US98-12764-5	Sequence 1, Appli
32	51.4	1.4	540	1	PCP-US98-12764-5	Sequence 1, Appli
33	51.4	1.4	824	52	US-60-207-458-11907	Sequence 18907, A
34	51	1.4	2241	13	US-08-913-196-3	Sequence 3, Appli
35	51	1.4	2241	16	US-08-205-048-3	Sequence 3, Appli
36	51	1.4	2367	13	US-08-913-196-1	Sequence 1, Appli
37	51	1.4	2367	16	US-08-205-048-1	Sequence 1, Appli
38	51	1.4	2394	12	US-08-827-556-730	Sequence 730, App
39	51	1.4	2394	14	US-09-036-082-1	Sequence 1, Appli
40	51	1.4	2394	23	US-09-611-529-506	Sequence 506, App
41	51	1.4	35014	12	US-08-831-156A-83	Sequence 83, Appli
42	51	1.4	47502	23	US-09-611-529-738	Sequence 7438, App
43	50.8	1.4	989	17	US-09-397-761A-729	Sequence 2729, App
44	50.8	1.4	7326	1	PCP-US98-26796-228	Sequence 228, App
45	50.6	1.4	1998	1	PCP-US98-26796-315	Sequence 345, App

ALIGNMENTS

OTHER INFORMATION: Description of Artificial Sequence: fusion of SbsA ; OTHER INFORMATION: and Male US-09-463-402-11

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 REFERENCE/DOCKET NUMBER: PM-0001-1P P
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 TELEFAX: (415) 845-4116
 INFORMATION FOR SEQ ID NO: 726:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 22306 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 IMMEDIATE SOURCE:
 CLONE: SAUIC726
 US-60-046-714-726